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RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/10/054,295

TIME: 15:49:16

Input Set : N:\CrF3\RULE60\10054295.raw

Output Set : N:\CRF3\02062002\J054295.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Cech, Thomas R.

6 Lingner, Joachim

7 Nakamura, Toru

8 Chapman, Karen B.

9 Morin, Gregg B.

10 Harley, Calvin

11 Andrews, William H.

13 (ii) TITLE OF INVENTION: Novel Telomerase

15 (iii) NUMBER OF SEQUENCES: 225

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Townsend and Townsend and Crew LLP

19 (B) STREET: Two Embarcadero Center, 8th Floor

20 (C) CITY: San Francisco

21 (D) STATE: California

22 (E) COUNTRY: United States of America

23 (F) ZIP: 94111

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/10/054,295

C--> 33 (B) FILING DATE: 18-Jan-2002

54 (C) CLASSIFICATION: 536

51 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: 08/854,050

38 (B) FILING DATE:

42 (A) APPLICATION NUMBER: US 08/846,017

43 (B) FILING DATE: 25-APR-1997

47 (A) APPLICATION NUMBER: US 08/844,419

48 (B) FILING DATE: 18-APR-1997

52 (A) APPLICATION NUMBER: US 08/724,643

53 (B) FILING DATE: 01-OCT-1996

56 (viii) ATTORNEY/AGENT INFORMATION:

57 (A) NAME: Apple, Randolph T.

58 (B) REGISTRATION NUMBER: 36,429

59 (C) REFERENCE/DOCKET NUMBER: 015389-002930US

61 (ix) TELECOMMUNICATION INFORMATION:

62 (A) TELEPHONE: (415) 576-0200

63 (B) TELEFAX: (415) 576-0300

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65 (2) INFORMATION FOR SEQ ID NO: 1:

67 (i) SEQUENCE CHARACTERISTICS:

68 (A) LENGTH: 3279 base pairs

69 (B) TYPE: nucleic acid

70 (C) STRANDEDNESS: single

71 (D) TOPOLOGY: linear

73 (ii) MOLECULE TYPE: other nucleic acid

74 (A) DESCRIPTION: /desc = "DNA"

76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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80	TTAATAAGCT	CAGATTTTAA	ATATTAATTA	CAAAACCTAA	ATGGAGGTTG	ATGTTGATAA	120
82	TCAAGCTGAT	AATCATGGCA	TTCACTCAGC	TCTTAAGACT	TGTGAAGAAA	TTAAAGAAGC	180
84	TAAAACGTTG	TACTCTTGGA	TCCAGAAAGT	TATTAGATGA	AGAAATCAAT	CTCAAAGTCA	240
86	TTATAAAGAT	TTAGAAGATA	TTAAAAATATT	TGCGCAGACA	AATATTGTTG	CTACTCCACG	300
88	AGACTATAAT	GAAGAAGATT	TTAAAGTTAT	TGCAAGAAAA	GAAGTATTTT	CAACTGGACT	360
90	AATGATCGAA	CTTATTGACA	AATGCTTAGT	TGAACTTCTT	TCATCAAGCG	ATGTTTCAGA	420
92	TAGACAAAAA	CTTCAATGAT	TTGGATTTC	ACTTAAGGGA	AATCAATTAG	CAAAGACCCA	480
94	TTTATTAACA	GCTCTTTC	CTCAAAAGCA	GTATTTCTTT	CAAGACGAAT	GGAACCAAGT	540
96	TAGAGCAATG	ATTGGAAATG	AGCTCTTCCG	ACATCTCTAC	ACTAAATATT	TAATATTCCA	600
98	GCGAACTTCT	GAAGGAACTC	TTGTTCAATT	TTGCGGGAAT	AACGTTTTTG	ATCATTTGAA	660
100	AGTCAACGAT	AAGTTTGACA	AAAAGCAAAA	AGGTGGAGCA	GCAGACATGA	ATGAACCTCG	720
102	ATGTTGATCA	ACCTGCAAA	ACAATGTCAA	GAATGAGAAA	GATCACTTTC	TCAACAACAT	780
104	CAACGTGCCG	AATTGGAATA	ATATGAAATC	AAGAACCAGA	ATATTTTATT	GCACTCATTT	840
106	TAATAGAAAT	AACCAATTCT	TCAAAAAGCA	TGAGTTTGTG	AGTAACAAAA	ACAATATTTT	900
108	AGCGATGGAC	AGAGCTCAGA	CGATATTCAC	GAATATATTC	AGATTTAATA	GAATTAGAAA	960
110	GAAGCTAAAA	GATAAGGTTA	TCGAAAAAAT	TGCCTACATG	CTTGAGAAAG	TCAAAGATTT	1020
112	TAACCTCAAC	TACTATTTAA	CAAAATCTTG	TCCTCTTCCA	GAAAATTGGC	GGGAACGGAA	1080
114	ACAAAAAATC	GAAAACCTGA	TAAATAAAAC	TAGAGAAGAA	AAGTCGAAGT	ACTATGAAGA	1140
116	GCTGTTTAGC	TACACAACCTG	ATAATAAATG	CGTCACACAA	TTTATTAATG	AATTTTCTTA	1200
118	CAATATACTC	CCCAAAGACT	TTTTGACTGG	AAGAAACCGT	AAGAATTTTC	AAAAGAAAGT	1260
120	TAAGAAATAT	GTGGAACATA	ACAAGCATGA	ACTCATTCAC	AAAAACTTAT	TGCTTGAGAA	1320
122	GATCAATACA	AGAGAAATAT	CATGGATGCA	GGTTGAGACC	TCTGCAAAGC	ATTTTTATTA	1380
124	TTTTGATCAC	GAAAACATCT	ACGTCTTATG	GAAATTGCTC	CGATGGATAT	TCGAGGATCT	1440
126	CGTCGTCTCG	CTGATTAGAT	GATTTTCTTA	TGTCACCGAG	CAACAGAAAA	GTTACTCCAA	1500
128	AACCTATTAC	TACAGAAAGA	ATATTTGGGA	CGTCATTATG	AAAATGTCAA	TCGCAGACTT	1560
130	AAAGAAGGAA	ACGCTTGCTG	AGGTCCAAGA	AAAAGAGGTT	GAAGAATGGA	AAAAGTCGCT	1620
132	TGGATTTGCA	CCTGGAAGAA	TCAGACTAAT	ACCGAAGAAA	ACTACTTTCC	GTCCAATTAT	1680
134	GACTTTCAAT	AAGAAGATTG	TAAATTCAGA	CCGGAAGACT	ACAAAATTAA	CTACAAATAC	1740
136	GAAGTTATTG	AACCTCTCACT	TAATGCTTAA	GACATTGAAG	AATAGAATGT	TTAAAGATCC	1800
138	TTTTGGATTG	GCTGTTTTTA	ACTATGATGA	TGTAATGAAA	AAGTATGAGG	AGTTTGTTTG	1860
140	CAAAATGGAAG	CAAGTTGGAC	AACCAAAACT	CTTCTTTGCA	ACTATGGATA	TCGAAAAGTG	1920
142	ATATGATAGT	GTAAACAGAG	AAAAACTATC	AACATTCCTA	AAAACTACTA	AATTACTTTC	1980
144	TTGAGATTTC	TGGATTATGA	CTGCACAAAT	TCTAAAGAGA	AAGAATAACA	TAGTTATCGA	2040
146	TTGCAAAAAC	TTTAGAAAGA	AAGAAATGAA	AGATTATTTT	AGACAGAAAT	TCCAGAAGAT	2100
148	TGCACTTGAA	GGAGGACAAT	ATCCAACCTT	ATTCAGTGTT	CTTGAAAATG	AACAAAATGA	2160
150	CTTAAATGCA	AAGAAAACAT	TAATTGTTGA	AGCAAAGCAA	AGAAATTATT	TTAAGAAAGA	2220
152	TAACCTACTT	CAACCAAGTCA	TTAATATTTG	CCAATATAAT	TACATTAAC	TTAATGGGAA	2280
154	GTTTTATAAA	CAACCAAAAG	GAATTCCTCA	AGGTCTTTGA	GTTTCATCAA	TTTTGTTCATC	2340
156	ATTTTATTAT	GCAACATTAG	AGGAAAGCTC	CTTAGGATTC	CTTAGAGATG	AATCAATGAA	2400

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158 CCCTGAAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC TTTTGATTAC 2460
160 AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAACTT ATAAACGTAA GTCGTGAAAA 2520
162 TGGATTTAAA TTCAATATGA AGAAACTACA GACTAGTTTT CCATTAAGTC CAAGCAAATT 2580
164 TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG 2640
166 GATTGGCATC TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT 2700
168 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT 2760
170 CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC CATTATTTTA GAAAGACGAT 2820
172 TACAACCGAA GACTTTGCGA ATAAACTCT CAACAAGTTA TTTATATCAG GCGGTTACAA 2880
174 ATACATGCAA TGAGCCAAAG AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG 2940
176 TATGATCGAC TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA 3000
178 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG ACTTTTTCTT 3060
180 TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA AAGTACATTT TCAACAGAGT 3120
182 TTGCATGATC CTCAAGGCAA AAGAAGCAAA GCTAAAAAGT GACCAATGTC AATCTCTAAT 3180
184 TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTGT 3240
186 TCTTATATAC TGGGGTTTTG GGGTTTTGGG GTTTTGGGG 3279

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188 (2) INFORMATION FOR SEQ ID NO: 2:

190 (i) SEQUENCE CHARACTERISTICS:

191 (A) LENGTH: 1031 amino acids

192 (B) TYPE: amino acid

193 (C) STRANDEDNESS: Not Relevant

W--> 194 (D) TOPOLOGY: Not Relevant

196 (ii) MOLECULE TYPE: protein

198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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200 Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
201 1 5 10 15
203 Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
204 20 25 30
206 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
207 35 40 45
209 Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
210 50 55 60
212 Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
213 65 70 75 80
215 Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
216 85 90 95
218 Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
219 100 105 110
221 Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
222 115 120 125
224 Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
225 130 135 140
227 Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
228 145 150 155 160
230 Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
231 165 170 175
233 Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
234 180 185 190
236 Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
237 195 200 205

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239   Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
240       210                      215                      220
242   Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
243       225                      230                      235                      240
245   Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
246       245                      250                      255
248   His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
249       260                      265                      270
251   Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
252       275                      280                      285
254   Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
255       290                      295                      300
257   Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
258       305                      310                      315                      320
260   Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
261       325                      330                      335
263   Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
264       340                      345                      350
266   Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
267       355                      360                      365
269   Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
270       370                      375                      380
272   Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
273       385                      390                      395                      400
275   Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
276       405                      410                      415
278   Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
279       420                      425                      430
281   Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
282       435                      440                      445
284   Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
285       450                      455                      460
287   Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
288       465                      470                      475                      480
290   Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
291       485                      490                      495
293   Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
294       500                      505                      510
296   Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
297       515                      520                      525
299   Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
300       530                      535                      540
302   Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
303       545                      550                      555                      560
305   Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
306       565                      570                      575
308   Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
309       580                      585                      590
311   Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr

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312																	
314	Asp	Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys	Thr	Thr	Lys	
315		610					615					620					
317	Leu	Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met	Thr	Ala	Gln	Ile	Leu	Lys	Arg	
318	625					630					635					640	
320	Lys	Asn	Asn	Ile	Val	Ile	Asp	Ser	Lys	Asn	Phe	Arg	Lys	Lys	Glu	Met	
321					645					650					655		
323	Lys	Asp	Tyr	Phe	Arg	Gln	Lys	Phe	Gln	Lys	Ile	Ala	Leu	Glu	Gly	Gly	
324				660					665					670			
326	Gln	Tyr	Pro	Thr	Leu	Phe	Ser	Val	Leu	Glu	Asn	Glu	Gln	Asn	Asp	Leu	
327		675					680					685					
329	Asn	Ala	Lys	Lys	Thr	Leu	Ile	Val	Glu	Ala	Lys	Gln	Arg	Asn	Tyr	Phe	
330		690					695					700					
332	Lys	Lys	Asp	Asn	Leu	Leu	Gln	Pro	Val	Ile	Asn	Ile	Cys	Gln	Tyr	Asn	
333	705					710					715					720	
335	Tyr	Ile	Asn	Phe	Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro	
336					725					730					735		
338	Gln	Gly	Leu	Cys	Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr	
339				740					745					750			
341	Leu	Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arg	Asp	Glu	Ser	Met	Asn	Pro	
342			755					760				765					
344	Glu	Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	
345		770					775					780					
347	Leu	Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	
348	785					790					795					800	
350	Ile	Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	
351					805					810					815		
353	Gln	Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys	Tyr	Gly	Met	
354				820					825					830			
356	Asp	Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile	
357			835					840					845				
359	Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn	
360		850					855					860					
362	Leu	Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	Thr	
363	865					870					875					880	
365	Lys	Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met	
366					885					890					895		
368	Asn	Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe	
369				900					905					910			

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L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:194 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2
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L:4574 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=99
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L:4815 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=102
L:4831 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=103
L:4846 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=104
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L:6706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176
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L:7300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
L:7743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7908 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217